

RECEIVED

APR 07 2003

TECH CENTER 1600/2000

1600

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/017,372E

DATE: 04/02/2003

TIME: 12:41:45

Input Set : A:\61302 Seq Listing.txt

Output Set: N:\CRF4\04022003\J017372E.raw

3 <110> APPLICANT: Wolfram, Lawrence A  
 4 Letterio, John J  
 6 <120> TITLE OF INVENTION: FUNCTIONALIZED TGF-BETA FUSION PROTEINS  
 8 <130> FILE REFERENCE: 4239-61302  
 10 <140> CURRENT APPLICATION NUMBER: US 10/017,372E  
 11 <141> CURRENT FILING DATE: 2001-10-19  
 13 <150> PRIOR APPLICATION NUMBER: US 60/242,292  
 14 <151> PRIOR FILING DATE: 2000-10-20  
 16 <160> NUMBER OF SEQ ID NOS: 39  
 18 <170> SOFTWARE: PatentIn version 3.2  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 28  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Artificial Sequence  
 25 <220> FEATURE:  
 26 <223> OTHER INFORMATION: Primer  
 28 <400> SEQUENCE: 1  
 29 ggagagatct ggtaccgaga tggcgctt 28  
 32 <210> SEQ ID NO: 2  
 33 <211> LENGTH: 42  
 34 <212> TYPE: DNA  
 35 <213> ORGANISM: Artificial Sequence  
 37 <220> FEATURE:  
 38 <223> OTHER INFORMATION: Primer  
 40 <400> SEQUENCE: 2  
 41 ataagaattg cggccgcttt aatcgatccc aagtgggctt gg 42  
 44 <210> SEQ ID NO: 3  
 45 <211> LENGTH: 48  
 46 <212> TYPE: DNA  
 47 <213> ORGANISM: Artificial Sequence  
 49 <220> FEATURE:  
 50 <223> OTHER INFORMATION: Primer  
 52 <400> SEQUENCE: 3  
 53 gactacaagg atgacgacga caaggccctg gataccaact actgcttc 48  
 56 <210> SEQ ID NO: 4  
 57 <211> LENGTH: 45  
 58 <212> TYPE: DNA  
 59 <213> ORGANISM: Artificial Sequence  
 61 <220> FEATURE:  
 62 <223> OTHER INFORMATION: Primer  
 64 <400> SEQUENCE: 4  
 65 cttgtcgtcg tcatccttgt agtctcggcg gtgccgggag ctgtg 45  
 68 <210> SEQ ID NO: 5

ENTERED

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/017,372E

DATE: 04/02/2003

TIME: 12:41:45

Input Set : A:\61302 Seq Listing.txt

Output Set: N:\CRF4\04022003\J017372E.raw

```

69 <211> LENGTH: 45
70 <212> TYPE: DNA
71 <213> ORGANISM: Artificial Sequence
73 <220> FEATURE:
74 <223> OTHER INFORMATION: Primer
76 <400> SEQUENCE: 5
77 gactacaagg atgacgacga caggagaaga actgctgcgt gcggc 45
80 <210> SEQ ID NO: 6
81 <211> LENGTH: 45
82 <212> TYPE: DNA
83 <213> ORGANISM: Artificial Sequence
85 <220> FEATURE:
86 <223> OTHER INFORMATION: Primer
88 <400> SEQUENCE: 6
89 cttgtcgtcg tcattcttgt agtctcggcg gtgccgggag ctgtg 45
92 <210> SEQ ID NO: 7
93 <211> LENGTH: 8
94 <212> TYPE: PRT
95 <213> ORGANISM: Artificial Sequence
97 <220> FEATURE:
98 <223> OTHER INFORMATION: Synthetic oligopeptide
100 <400> SEQUENCE: 7
102 Asp Tyr Lys Asp Asp Asp Asp Lys
103 1 5
106 <210> SEQ ID NO: 8
107 <211> LENGTH: 1197
108 <212> TYPE: DNA
109 <213> ORGANISM: Artificial Sequence
111 <220> FEATURE:
112 <223> OTHER INFORMATION: Porcine (Sus scrofa) TGF-beta1/N-terminal FLAG Fusion
Construct
115 <220> FEATURE:
116 <221> NAME/KEY: CDS
117 <222> LOCATION: (1)..(1197)
118 <223> OTHER INFORMATION: Protein coding sequence
120 <220> FEATURE:
121 <221> NAME/KEY: misc_feature
122 <222> LOCATION: (278)..(279)
123 <223> OTHER INFORMATION: Maturation cleavage site (relates to amino acid residue
nos.)
125 <400> SEQUENCE: 8
126 atg gcg cct tcg ggg ctg cgg ctc ttg ccg ctg ctg ctg ccg ctg ctg 48
127 Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
128 1 5 10 15
130 tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc gga ctg tcc acc 96
131 Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
132 20 25 30
134 tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc atc gag gcc 144
135 Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
136 35 40 45
138 att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc ccc ccg agc 192

```

## RAW SEQUENCE LISTING

DATE: 04/02/2003

PATENT APPLICATION: US/10/017,372E

TIME: 12:41:45

Input Set : A:\61302 Seq Listing.txt

Output Set: N:\CRF4\04022003\J017372E.raw

139	Ile	Arg	Gly	Gln	Ile	Leu	Ser	Lys	Leu	Arg	Leu	Ala	Ser	Pro	Pro	Ser	
140		50					55					60					
142	cag	ggg	gac	gtg	ccg	ccc	ggc	ccg	ctg	cct	gag	gca	gta	ctg	gct	ctt	240
143	Gln	Gly	Asp	Val	Pro	Pro	Gly	Pro	Leu	Pro	Glu	Ala	Val	Leu	Ala	Leu	
144	65					70					75					80	
146	tac	aac	agt	acc	cgc	gac	cgg	gta	gcc	ggg	gaa	agt	gtc	gaa	ccg	gag	288
147	Tyr	Asn	Ser	Thr	Arg	Asp	Arg	Val	Ala	Gly	Glu	Ser	Val	Glu	Pro	Glu	
148					85					90					95		
150	ccc	gag	cca	gag	gcg	gac	tac	tac	gcc	aag	gag	gtc	acc	cgc	gtg	cta	336
151	Pro	Glu	Pro	Glu	Ala	Asp	Tyr	Tyr	Ala	Lys	Glu	Val	Thr	Arg	Val	Leu	
152				100					105					110			
154	atg	gtg	gaa	agc	ggc	aac	caa	atc	tat	gat	aaa	ttc	aag	ggc	acc	ccc	384
155	Met	Val	Glu	Ser	Gly	Asn	Gln	Ile	Tyr	Asp	Lys	Phe	Lys	Gly	Thr	Pro	
156			115					120					125				
158	cac	agc	tta	tat	atg	ctg	ttc	aac	acg	tcg	gag	ctc	cgg	gaa	gcg	gtg	432
159	His	Ser	Leu	Tyr	Met	Leu	Phe	Asn	Thr	Ser	Glu	Leu	Arg	Glu	Ala	Val	
160		130					135					140					
162	ccg	gaa	cct	gta	ttg	ctc	tct	cgg	gca	gag	ctg	cgc	ctg	ctg	agg	ctc	480
163	Pro	Glu	Pro	Val	Leu	Leu	Ser	Arg	Ala	Glu	Leu	Arg	Leu	Leu	Arg	Leu	
164	145				150					155					160		
166	aag	tta	aaa	gtg	gag	cag	cac	gtg	gag	cta	tac	cag	aaa	tac	agc	aat	528
167	Lys	Leu	Lys	Val	Glu	Gln	His	Val	Glu	Leu	Tyr	Gln	Lys	Tyr	Ser	Asn	
168				165					170					175			
170	gat	tcc	tgg	cgc	tac	ctc	agc	aac	cgg	ctg	ctg	gcc	ccc	agt	gac	tca	576
171	Asp	Ser	Trp	Arg	Tyr	Leu	Ser	Asn	Arg	Leu	Leu	Ala	Pro	Ser	Asp	Ser	
172			180						185					190			
174	ccg	gag	tgg	ctg	tcc	ttt	gat	gtc	acc	gga	gtt	gtg	cgg	cag	tgg	ctg	624
175	Pro	Glu	Trp	Leu	Ser	Phe	Asp	Val	Thr	Gly	Val	Val	Arg	Gln	Trp	Leu	
176			195					200					205				
178	acc	cgc	aga	gag	gct	ata	gag	ggg	ttt	cgc	ctc	agt	gcc	cac	tct	tcc	672
179	Thr	Arg	Arg	Glu	Ala	Ile	Glu	Gly	Phe	Arg	Leu	Ser	Ala	His	Ser	Ser	
180		210					215					220					
182	tct	gac	agc	aaa	gat	aac	aca	ctc	cac	gtg	gaa	att	aac	ggg	ttc	aat	720
183	Ser	Asp	Ser	Lys	Asp	Asn	Thr	Leu	His	Val	Glu	Ile	Asn	Gly	Phe	Asn	
184	225				230					235					240		
186	tct	ggc	cgc	cgg	ggg	gac	ctg	gcc	acc	att	cac	ggc	atg	aac	cgg	ccc	768
187	Ser	Gly	Arg	Arg	Gly	Asp	Leu	Ala	Thr	Ile	His	Gly	Met	Asn	Arg	Pro	
188				245					250					255			
190	ttc	ctg	ctc	ctc	atg	gcc	acc	ccg	ctg	gag	agg	gcc	cag	cac	ctg	cac	816
191	Phe	Leu	Leu	Leu	Met	Ala	Thr	Pro	Leu	Glu	Arg	Ala	Gln	His	Leu	His	
192				260					265					270			
194	agc	tcc	cgg	cac	cgc	cga	gac	tac	aag	gat	gac	gac	gac	aag	gcc	ctg	864
195	Ser	Ser	Arg	His	Arg	Arg	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Ala	Leu	
196			275					280					285				
198	gat	acc	aac	tac	tgc	ttc	agc	tcc	acg	gag	aag	aac	tgc	tgc	gtg	cgg	912
199	Asp	Thr	Asn	Tyr	Cys	Phe	Ser	Ser	Thr	Glu	Lys	Asn	Cys	Cys	Val	Arg	
200		290					295					300					
202	cag	ctc	tac	att	gac	ttc	cgg	aag	gac	ctg	ggc	tgg	aag	tgg	att	cat	960
203	Gln	Leu	Tyr	Ile	Asp	Phe	Arg	Lys	Asp	Leu	Gly	Trp	Lys	Trp	Ile	His	

## RAW SEQUENCE LISTING

DATE: 04/02/2003

PATENT APPLICATION: US/10/017,372E

TIME: 12:41:45

Input Set : A:\61302 Seq Listing.txt

Output Set: N:\CRF4\04022003\J017372E.raw

```

204 305          310          315          320
206 gaa ccc aag ggc tac cat gcc aat ttc tgc ctg ggg ccc tgt ccc tac      1008
207 Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
208          325          330          335
210 atc tgg agc cta gac act cag tac agc aag gtc ctg gct ctg tac aac      1056
211 Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
212          340          345          350
214 cag cac aac ccg ggc gcg tcg gcg gcg ccg tgc tgc gtg ccg cag gcg      1104
215 Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
216          355          360          365
218 ctg gag cca ctg ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg      1152
219 Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
220          370          375          380
222 gag cag ctg tcc aac atg atc gtg cgt tcc tgc aag tgc agc tga      1197
223 Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
224 385          390          395
227 <210> SEQ ID NO: 9
228 <211> LENGTH: 398
229 <212> TYPE: PRT
230 <213> ORGANISM: Artificial Sequence
232 <220> FEATURE:
233 <223> OTHER INFORMATION: Porcine (Sus scrofa) TGF-betal/N-terminal FLAG Fusion
Construct
235 <400> SEQUENCE: 9
237 Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
238 1          5          10          15
241 Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
242          20          25          30
245 Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
246          35          40          45
249 Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
250          50          55          60
253 Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
254 65          70          75          80
257 Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
258          85          90          95
261 Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
262          100         105         110
265 Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
266          115         120         125
269 His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
270          130         135         140
273 Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
274 145         150         155         160
277 Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
278          165         170         175
281 Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
282          180         185         190
285 Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
286          195         200         205

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/017,372E

DATE: 04/02/2003

TIME: 12:41:45

Input Set : A:\61302 Seq Listing.txt

Output Set: N:\CRF4\04022003\J017372E.raw

```

289 Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
290      210                      215                      220
293 Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
294 225                      230                      235                      240
297 Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
298                      245                      250                      255
301 Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
302                      260                      265                      270
305 Ser Ser Arg His Arg Arg Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu
306                      275                      280                      285
309 Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg
310      290                      295                      300
313 Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His
314 305                      310                      315                      320
317 Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
318                      325                      330                      335
321 Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
322                      340                      345                      350
325 Gln His Asn Pro Gly Ala Ser Ala Pro Cys Cys Val Pro Gln Ala
326                      355                      360                      365
329 Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
330      370                      375                      380
333 Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
334 385                      390                      395

```

337 &lt;210&gt; SEQ ID NO: 10

338 &lt;211&gt; LENGTH: 363

339 &lt;212&gt; TYPE: DNA

340 &lt;213&gt; ORGANISM: Artificial Sequence

342 &lt;220&gt; FEATURE:

343 &lt;223&gt; OTHER INFORMATION: Porcine (Sus scrofa) TGF-beta1/N-terminal FLAG Fusion

## Construct

345 &lt;400&gt; SEQUENCE: 10

```

346 gactacaagg atgacgacga caaggccctg gataccaact actgcttcag ctccacggag      60
348 aagaactgct gcgtgcggca gctctacatt gacttcgga aggacctggg ctggaagtgg      120
350 attcatgaac ccaagggtta ccatgccaat ttctgcctgg ggccctgtcc ctacatctgg      180
352 agcctagaca ctcatgacag caaggctcctg gctctgtaca accagcacia cccgggagcg      240
354 tcggcgagcg cgtgctgcgt gccgcaggcg ctggagccac tgcccatcgt gtactacgtg      300
356 ggccgcaagc ccaagggtga gcagctgtcc aacatgatcg tgcgttcctg caagtgcagc      360
358 tga                                          363

```

361 &lt;210&gt; SEQ ID NO: 11

362 &lt;211&gt; LENGTH: 120

363 &lt;212&gt; TYPE: PRT

364 &lt;213&gt; ORGANISM: Artificial Sequence

366 &lt;220&gt; FEATURE:

367 &lt;223&gt; OTHER INFORMATION: Porcine (Sus scrofa) TGF-beta1/N-terminal FLAG Fusion

## Construct

370 &lt;220&gt; FEATURE:

371 &lt;221&gt; NAME/KEY: PEPTIDE

372 &lt;222&gt; LOCATION: (1)..(8)

373 &lt;223&gt; OTHER INFORMATION: FLAG tag

375 &lt;400&gt; SEQUENCE: 11

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/017,372E

DATE: 04/02/2003

TIME: 12:41:46

Input Set : A:\61302 Seq Listing.txt

Output Set: N:\CRF4\04022003\J017372E.raw